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Reviewer: Anne Corrigan

Timestamp: Thu May 03 14:46:20 EDT 2007

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Application No: 10585464

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Input Set:

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Started: 2007-05-03 14:46:12.425

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Total Warnings: 0

Total Errors: 0

No. of SeqIDs Defined: 1

Actual SeqID Count: 1

ErrCode	Error Description
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SEQUENCE LISTING

<110> Moses, Marsha A.
Roy, Roopali

<120> METHODS FOR DIAGNOSIS AND PROGNOSIS OF CANCERS OF
EPITHELIAL ORIGIN

<130> CMC-011

<140> 10585464

<141> 2006-07-07

<150> PCT/US05/00714

<151> 2005-01-10

<150> 60/535,306

<151> 2004-01-09

<160> 1

<170> PatentIn Ver. 3.3

<210> 1

<211> 909

<212> PRT

<213> Homo sapiens

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Leu	Trp	Asn	Gln	Gly	Arg	Ala	Asp	Glu	Val	Val	Ser	Ala	Ser	Val	Arg
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Ser	Gly	Asp	Leu	Trp	Ile	Pro	Val	Lys	Ser	Phe	Asp	Ser	Lys	Asn	His
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Pro	Glu	Val	Leu	Asn	Ile	Arg	Leu	Gln	Arg	Glu	Ser	Lys	Glu	Leu	Ile
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Ile	Asn	Leu	Glu	Arg	Asn	Glu	Gly	Leu	Ile	Ala	Ser	Ser	Phe	Thr	Glu
			85					90						95	

Thr	His	Tyr	Leu	Gln	Asp	Gly	Thr	Asp	Val	Ser	Leu	Ala	Arg	Asn	Tyr
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Thr	Val	Ile	Leu	Gly	His	Cys	Tyr	Tyr	His	Gly	His	Val	Arg	Gly	Tyr
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Ser	Asp	Ser	Ala	Val	Ser	Leu	Ser	Thr	Cys	Ser	Gly	Leu	Arg	Gly	Leu
	130					135					140				

Ile	Val	Phe	Glu	Asn	Glu	Ser	Tyr	Val	Leu	Glu	Pro	Met	Lys	Ser	Ala
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145		150		155		160
Thr Asn Arg Tyr Lys Leu Phe Pro Ala Lys Lys Leu Lys Ser Val Arg						
	165		170		175	
Gly Ser Cys Gly Ser His His Asn Thr Pro Asn Leu Ala Ala Lys Asn						
	180		185		190	
Val Phe Pro Pro Pro Ser Gln Thr Trp Ala Arg Arg His Lys Arg Glu						
	195		200		205	
Thr Leu Lys Ala Thr Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn						
	210		215		220	
Arg Glu Phe Gln Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg						
225		230		235		240
Leu Ile Glu Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn						
	245		250		255	
Ile Arg Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys						
	260		265		270	
Cys Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp						
	275		280		285	
Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala Gln						
	290		295		300	
Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met Ala Pro						
305		310		315		320
Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile Val Met Asp						
	325		330		335	
His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu Ala His Glu Leu						
	340		345		350	
Gly His Asn Phe Gly Met Asn His Asp Thr Leu Asp Arg Gly Cys Ser						
	355		360		365	
Cys Gln Met Ala Val Glu Lys Gly Gly Cys Ile Met Asn Ala Ser Thr						
	370		375		380	
Gly Tyr Pro Phe Pro Met Val Phe Ser Ser Cys Ser Arg Lys Asp Leu						
385		390		395		400
Glu Thr Ser Leu Glu Lys Gly Met Gly Val Cys Leu Phe Asn Leu Pro						
	405		410		415	
Glu Val Arg Glu Ser Phe Gly Gly Gln Lys Cys Gly Asn Arg Phe Val						
	420		425		430	
Glu Glu Gly Glu Glu Cys Asp Cys Gly Glu Pro Glu Glu Cys Met Asn						
	435		440		445	
Arg Cys Cys Asn Ala Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys						

450		455		460	
Ala His Gly Leu Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr					
465		470		475	480
Ala Cys Arg Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr					
	485		490		495
Gly Ala Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His					
	500		505		510
Ser Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys Gln Thr					
	515		520		525
His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys Pro Ala					
	530		535		540
Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro Tyr Gly					
545		550		555	560
Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys Glu Met Arg					
	565		570		575
Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly Ala Ser Arg Pro					
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Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr Asn Ile Pro Leu Gln					
	595		600		605
Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr His Val Tyr Leu Gly Asp					
	610		615		620
Asp Met Pro Asp Pro Gly Leu Val Leu Ala Gly Thr Lys Cys Ala Asp					
625		630		635	640
Gly Lys Ile Cys Leu Asn Arg Gln Cys Gln Asn Ile Ser Val Phe Gly					
	645		650		655
Val His Glu Cys Ala Met Gln Cys His Gly Arg Gly Val Cys Asn Asn					
	660		665		670
Arg Lys Asn Cys His Cys Glu Ala His Trp Ala Pro Pro Phe Cys Asp					
	675		680		685
Lys Phe Gly Phe Gly Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala					
	690		695		700
Asp Asn Gln Gly Leu Thr Ile Gly Ile Leu Val Thr Ile Leu Cys Leu					
705		710		715	720
Leu Ala Ala Gly Phe Val Val Tyr Leu Lys Arg Lys Thr Leu Ile Arg					
	725		730		735
Leu Leu Phe Thr Asn Lys Lys Thr Thr Ile Glu Lys Leu Arg Cys Val					
	740		745		750
Arg Pro Ser Arg Pro Pro Arg Gly Phe Gln Pro Cys Gln Ala His Leu					

755

760

765

Gly His Leu Gly Lys Gly Leu Met Arg Lys Pro Pro Asp Ser Tyr Pro
770 775 780

Pro Lys Asp Asn Pro Arg Arg Leu Leu Gln Cys Gln Asn Val Asp Ile
785 790 795 800

Ser Arg Pro Leu Asn Gly Leu Asn Val Pro Gln Pro Gln Ser Thr Gln
805 810 815

Arg Val Leu Pro Pro Leu His Arg Ala Pro Arg Ala Pro Ser Val Pro
820 825 830

Ala Arg Pro Leu Pro Ala Lys Pro Ala Leu Arg Gln Ala Gln Gly Thr
835 840 845

Cys Lys Pro Asn Pro Pro Gln Lys Pro Leu Pro Ala Asp Pro Leu Ala
850 855 860

Arg Thr Thr Arg Leu Thr His Ala Leu Ala Arg Thr Pro Gly Gln Trp
865 870 875 880

Glu Thr Gly Leu Arg Leu Ala Pro Leu Arg Pro Ala Pro Gln Tyr Pro
885 890 895

His Gln Val Pro Arg Ser Thr His Thr Ala Tyr Ile Lys
900 905